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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=25; hr=16; min=0; sec=30; ms=961;]

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Application No: 10554076 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-02-13 11:08:42.204
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Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

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Input Set:

Output Set:

Started: 2008-02-13 11:08:40.414
Finished: 2008-02-13 11:08:42.204
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 790 ms
Total Warnings: 29
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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SEQUENCE LISTING

<110> Leppla, Stephen H.
Avallone, Jennifer
Bugge, Thomas
Liu, Shi-Hui
Osorio, Manuel
The Government of the United States of America
as represented by The Secretary of the
Department of Health and Human Services

<120> Activation of Recombinant Diphtheria Toxin Fusion
Proteins by Specific Proteases Highly Expressed on the
Surface of Tumor Cells

<130> 015280-478100US

<140> 10554076
<141> 2008-02-13

<150> US 60/468,577
<151> 2003-05-06

<150> WO PCT/US04/14306
<151> 2004-05-06

<160> 30

<170> PatentIn Ver. 2.1

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<223> signal sequence

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DTGM-L1
DT-GMCSF fusion protein in which native furin
recognition cleavage site replaced by matrix
metalloproteinase (MMP) recognition cleavage site

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1566

<210> 3

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DTGM-L2

DT-GMCSF fusion protein in which native furin
recognition cleavage site replaced by matrix
metalloproteinase (MMP) recognition cleavage site

<400> 3

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tctggcacac aaggaaatta tgacgtatgtatggaaagggt tttatagtac cgacaataaa 180
tacgacgctg cgggataactc ttagataat gaaaaccgcg tctctggaaa agctggaggc 240
gtggtcaaag tgacgtatcc aggactgacg aaggttctcg cactaaaagt ggataatgcc 300
gaaactatttta agaaagagtt aggttaagt ctcaactgaac cggttatggc gcaagtccg 360
acggaaagagt ttatcaaaag gttcggtat ggtgctcgc gtgtatgtct cagccttccc 420
ttcgctgagg ggagttcttag cgttgaatat attaataact gggAACAGGC gaaagcgtta 480
agcgtagaac ttgagattaa ttttggaaacc cgtggaaaac gtggccaaga tgcgatgtat 540
gagtatatgg ctcaagcctg tgcaggaaat ggaccattag gattatggc acaaggtagc 600
tcattgtcat gcataaatct tgattggat gtcataaggg ataaaaactaa gacaaagata 660
gagtcttga aagagcatgg ccctatcaaa aataaaatga gcgaaagtcc caataaaaaca 720
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1566

<210> 4

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DTGM-U2 DT-GMCSF fusion
protein in which native furin recognition cleavage site
replaced by urokinase-type plasminogen activator (uPA)
recognition cleavage site

<400> 4

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taccacggga ctaaacctgg ttatgtat tccattcaaa aaggtataca aaagccaaaa 120
tctggcac ac aaggaaatta tgacgatgat tggaaagggt tttatagtac cgacaataaa 180
tacgacgctg cgggataactc ttagataat gaaaacccgc tctctggaaa agctggaggc 240
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gaaactatta agaaagagtt aggttaagt ctcaactgaac cgttgatgga gcaagtccga 360
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gagttatgg ctcaagcctg tgcaggaaat ggaagtggaa gatcagcagg tagctcattg 600
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ttgaaagagc atggccctat caaaaataaa atgagcggaa gtcggcaataa aacagtatct 720
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<210> 5
<211> 1560
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DTGM-U3 DT-GM-CSF fusion
protein in which native furin recognition cleavage site
replaced by urokinase-type plasminogen activator (uPA)
recognition cleavage site

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DTEGF-L1 DT-EGF
fusion protein in which native furin recognition
cleavage site replaced by matrix metalloproteinase
(MMP) recognition cleavage site

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DTEGF-L2 DT-EGF
fusion protein in which native furin recognition
cleavage site replaced by matrix metalloproteinase
(MMP) recognition cleavage site

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<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DTEGF-U2 DT-EGF fusion
protein in which native furin recognition cleavage site
replaced by urokinase-type plasminogen activator (uPA)
recognition cleavage site

<400> 8

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tctggtacac aaggaaatta tgacgtatgat tggaaagggt tttatagtac cgacaataaa 180
tacgacgctg cgggatactc ttagataat gaaaacccgc tctctggaaa agctggaggc 240
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